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OM protein - protein search, using swi/model

Run on: June 25, 2003, 14:20:45 ; Search time 5.45349 Seconds

(Without alignments)  
798.574 Million cell updates/sec

Title: US-09-622-613b-8

Perfect score: 582  
Sequence: 1 MODMLFFOKKHLNTRDVC.....TFCVTCENQAPVHEVGVC 105

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt.40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	538	92.4	104	1	RN30_RANPI
2	277	47.6	111	1	RNPO_RANCA
3	270.5	46.5	111	1	LECS_RANCA
4	254.5	43.7	111	1	RNPL_RANCA
5	139	23.9	119	1	RNP_IGUIG
6	121.5	20.9	145	1	ANGR_MOUSE
7	121.5	20.9	146	1	ANGI_CERAE
8	120	20.6	124	1	RNP_CALMU
9	117	20.1	148	1	ANGI_BOVIN
10	115	19.8	128	1	RNPB_CAVPO
11	114	19.6	128	1	RNP_MYOCO
12	113	19.4	124	1	RNP_BALAC
13	112.5	19.3	146	1	ANGI_MACMU
14	109.5	18.8	145	1	ANGI_MOUSE
15	109.5	18.8	146	1	ANGI_PAPHA
16	108	18.6	128	1	RNP_PROGU
17	107.5	18.5	155	1	ECBP4_MOUSE
18	107	18.4	125	1	ANGI_RABIT
19	107	18.4	128	1	RNP_HYDHY
20	107	18.4	146	1	ANGI_MITOA
21	105.5	18.1	147	1	RNLA_HUMAN
22	105	18.0	124	1	RNP_CHIBR
23	105	18.0	150	1	RNP_BOVIN
24	104	17.9	156	1	ECBP3_MOUSE
25	103	17.7	147	1	ANGI_HUMAN
26	103	17.7	147	1	ANGI_PANTR
27	102	17.5	124	1	RNP_AEPMF
28	102	17.5	124	1	RNP_ANTAM
29	102	17.5	124	1	RNP_HIPAM
30	102	17.5	124	1	RNP_SHEEP
31	101.5	17.4	123	1	ANGI_PIG
32	101.5	17.4	150	1	RNK6_SATSC
33	101	17.4	124	1	RNP_BOBBU

34	101	17.4	124	1	RNP_CONTA	P00660 conchochaete
35	101	17.4	124	1	RNP_GAZTH	P07848 gazella tho
36	100	17.2	123	1	ANG2_BOVIN	P80929 bos taurus
37	100	17.2	124	1	RNP_GIRCA	P00662 giraffa cam
38	100	17.2	124	1	RNP_PIG	P00671 sus scrofa
39	100	17.2	128	1	RNP_HYSCR	P04060 hystrix cri
40	100	17.2	156	1	RNP_MYOGI	O9wus1 myoxus glis
41	100	17.2	167	1	RNBR_BOVIN	P39873 bos taurus
42	99	17.0	124	1	RNP_CAMDR	P00670 camelus dro
43	99	17.0	128	1	RNP_HORSE	P00674 equus caball
44	99	17.0	146	1	ANGI_SAGO	O8wne2 sequinus oe
45	98.5	16.9	155	1	ECPL_MOUSE	P97426 mus musculus

## ALIGNMENTS

RESULT 1	ID	RN30_RANPI	STANDARD:	PRT:	104 AA.
AC	P22069:				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	01-FEB-1995 (Rel. 31, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OC	Rana pipiens (Northern leopard frog).				
OC	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:				
OC	Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae: Rana:				
OX	NCBI_TaxID=8404;				
RN	[1]				
RP	SEQUENCE.				
RP	TISSUE=Embryo:				
RX	MEDLINE=91093131; PubMed=1985896;				
RA	Ardelt W., Mikulski S.M., Shogen K.:				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens				
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251(1991).				
RN	[2]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=93066156; PubMed=1438177;				
RA	Moslimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,				
RT	James M.N.G.:				
RT	"Comparative molecular modeling and crystallization of P-30				
RT	protein: a novel antitumor protein of Rana pipiens oocytes and early				
RT	embryos.";				
RL	Proteins 14:392-400(1992).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RX	MEDLINE=94166079; PubMed=8120892;				
RA	Moslimann S.C., Ardelt W., James M.N.G.:				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an				
RT	amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY				
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR				
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH				
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.				
DR	PDB: 1ONC; 31-JAN-94.				
DR	InterPro: IPR001427; RNaseA.				
DR	Pfam: PF00074; RNaseA; 1.				
DR	Prodom: PD000535; RNaseA; 1.				
DR	SMART: SM00092; RNase_Pc; 1.				
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.				
FT	MOD_RES	1	10	1	PYRROLIDONE CARBOXYLIC ACID.
FT	ACT_SITE	31	31		
FT	ACT_SITE	97	97		
FT	DISULFID	19	68		
FT	DISULFID	30	75		
FT	DISULFID	48	90		

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FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA: 11845 MW: 22A753C2F9E566B4 CRC64;

Query Match 92.4%; Score 538; DB 1; Length 104;
Best Local Similarity 93.3%; Pred. No. 1e-51;
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKNVLT 61
DB 1 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKNVLT 60
OY 62 FEFYLSDCNVTSPCKYKLTSTIFCYTCENQAPVHVGHC 105
DB 61 SFEYLSDCNVTSPCKYKLTSTNKFVCYTCENQAPVHVGVC 104

RESULT 2
RNPO_RANCA STANDARD; PRT: 111 AA.
ID RNPO_RANCA
AC P11916:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallic acid-binding
DE lectin) (SBL-C).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN 11
RP TISSUE=Egg;
RC MEDLINE=87299649; PubMed=3304421;
RA Tiltani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of stallic acid binding lectin from frog (Rana
RL catesbeiana) eggs."
RL Biochemistry 26:2189-2194(1987).
RN 12
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373337;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RL catesbeiana (bullfrog) oocytes."
RL Nucleic Acids Res. 20:1371-1377(1992).
RN 13
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Tiltani K.;
RT "Ribonuclease activity of stallic acid-binding lectin from Rana
RL catesbeiana eggs."
RL Glycobiology 3:37-45(1993).
RN 14
RP STRUCTURE BY NMR.
RX MEDLINE=86437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;

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RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).".
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
CC RESIDUES WITH A 3'FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
CC AS SUBSTRATES, AND PREFERENCES THE FORMER. THE S-LECTINS IN FROG EGGS
CC MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG
CC EMBRYO. THIS LECTIN AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING
CC NORMAL LYMPHOCYTES, ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND
CC HUMAN ORIGIN.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A27121; A27121.
DR PDB: 1BC4; 28-OCT-98.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA.
DR ProDom: PD000535; RNaseA.
DR SMART: SM00092; RNase_Pc.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; stallic acid; lectin; 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
SQ SEQUENCE 111 AA: 12464 MW: 0BC9E5F5729ECF4 CRC64;

Query Match 47.6%; Score 277; DB 1; Length 111;
Best Local Similarity 47.7%; Pred. No. 2.3e-23;
Matches 53; Conservative 16; Mismatches 34; Indels 8; Gaps 3;

OY 2 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKN 57
DB 1 QWMLTFQKKHLNTRDVCNMLSTNLFHCKDKNTFIYSRPEPVKAICGIIASKN 59
OY 58 VTFEFYLSDC---NVTSPCKYKLTSTIFCYTCENQAPVHVGHC 105
DB 60 VLTTRFQNLCTKRISITPRCPYSSKRTETNYICVKENQAPVHVGIGRC 110

RESULT 3
LECS_RANJA STANDARD; PRT: 111 AA.
ID LECS_RANJA
AC P18839:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stallic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN 11
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamliya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Tiltani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RL eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: JX0120; JX0120.

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DR HSSP: P11916; 1BC4  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin.  
 FT MOD\_RES 1 1  
 FT ACT\_SITE 10 10 BY SIMILARITY.  
 FT ACT\_SITE 35 35 BY SIMILARITY.  
 FT ACT\_SITE 103 103 BY SIMILARITY.  
 FT DISULFID 19 72  
 FT DISULFID 34 82  
 FT DISULFID 52 97  
 FT DISULFID 94 111  
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 46.58; Score 270.5; DB 1; Length 111;  
 Best Local Similarity 43.28; Pred. No. 1,2e-22;  
 Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

QY 2 QDMVTFQKHLTNRDVCNNILSTNLF---HCKDKNTFLYSRPEPVKATCKGIASKN 57  
 1 QNNAKFOEKHIDPNTSNCNTIMDKSIYVGCKEKNTFLISSATTVKAICSGASTNRN 60  
 DB 58 VLTTFEFLSDC---NNTSRPKYKLLKSTITFCVTCENQAPVHFVGVGHC 105  
 61 VLTTRQLNTCIRSATAPRCPYNSRTETNVICVCKENLPIVHFAIGRC 111

RESULT 4  
 RNP\_LANCA STANDARD; PRT: 111 AA.  
 ID RNP\_LANCA  
 AC P14626;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease, liver (EC 3.1.27.5).  
 OS Rana catesbeiana (Bull frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.  
 OC NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Liver;  
 RX MEDLINE=90130374; Pubmed=2613682;  
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,  
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.";  
 RL J. Biochem. 106:729-735(1989).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSSP: P11516; 1BC4.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT MOD\_RES 1 1  
 FT ACT\_SITE 10 10 PYROLIDONE CARBOXYLIC ACID.  
 FT ACT\_SITE 35 35 BY SIMILARITY.  
 FT ACT\_SITE 104 104 BY SIMILARITY.  
 FT DISULFID 19 72 BY SIMILARITY.  
 FT DISULFID 34 82 BY SIMILARITY.  
 FT DISULFID 52 97 BY SIMILARITY.  
 FT DISULFID 94 111 PROBABLE.  
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 43.7%; Score 254.5; DB 1; Length 111;  
 Best Local Similarity 41.44; Pred. No. 6,3e-21;  
 Matches 46; Conservative 19; Mismatches 39; Indels 7; Gaps 2;

QY 2 QDMVTFQKHLTNRDVCNNILSTNLF---HCKDKNTFLYSRPEPVKATCKGIASKN 57  
 1 QNNAKFOEKHIDPNTSNCNTIMDKSIYVGCKEKNTFLISSATTVKAICSGASTNRN 60  
 DB 58 VLTTFEFLSDC---NNTSRPKYKLLKSTITFCVTCENQAPVHFVGVGHC 105  
 61 ELSTTSFKLNTCIRDSITPRCPYPSPDNKKICVCKEKLPIVHFAIGRC 111

RESULT 5  
 RNP\_IGUG STANDARD; PRT: 119 AA.  
 ID RNP\_IGUG  
 AC P80287;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).  
 OS Iguana iguana (Common Iguana).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidosaurs; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.  
 OC NCBI\_TaxID=8517;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Pancreas;  
 RX MEDLINE=94139745; Pubmed=8307028;  
 RA Zhao W., Beintema J.J., Hofsteenge J.;  
 RT "The amino acid sequence of Iguana (Iguana iguana) pancreatic ribonuclease.";  
 RL Eur. J. Biochem. 219:641-646(1994).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: PANCREAS.  
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
 DR HSSP: P00656; 1LSQ.  
 DR InterPro: IPR001427; RNaseA.  
 DR Pfam: PF00074; RNaseA: 1.  
 DR PRINTS: PR00794; RIBONUCLEASE.  
 DR ProDom: PD000535; RNaseA: 1.  
 DR SMART: SM00092; RNase\_Pc: 1.  
 DR PROSITE: PS00127; RNase\_PANCREATIC; 1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT MOD\_RES 1 1  
 FT DISULFID 25 80 PYROLIDONE CARBOXYLIC ACID.  
 FT DISULFID 39 91 BY SIMILARITY.  
 FT DISULFID 57 106 BY SIMILARITY.  
 FT ACT\_SITE 10 10 BY SIMILARITY.  
 FT ACT\_SITE 40 40 BY SIMILARITY.  
 FT ACT\_SITE 113 113 BY SIMILARITY.  
 SQ SEQUENCE 119 AA; 13324 MW; 6072PFB5B7B15BD5A CRC64;

Query Match 23.9%; Score 139; DB 1; Length 119;  
 Best Local Similarity 29.8%; Pred. No. 2,3e-08;  
 Matches 34; Conservative 19; Mismatches 45; Indels 16; Gaps 5;

QY 2 QDMVTFQKHLTNRDVCNNILSTNLF---HCKDKNTFLYSRPEPVKATCKGIASKN 57  
 1 QNNAKFOEKHIDPNTSNCNTIMDKSIYVGCKEKNTFLISSATTVKAICSGASTNRN 60  
 DB 51 GIASKNVLTTFEFLSDC---NNTSRPKYKLLKSTITFCVTCENQAPVH 99  
 61 GTHVEDMAYDSNESFDLTDCKNVGGTAPSSCKYNGTGTRIRIACENQPVH 114

RESULT 6  
 ANGR\_MOUSE STANDARD; PRT: 145 AA.  
 ID ANGR\_MOUSE

AC 064438;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Angiogenin-related protein precursor.  
GN ANGRP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129; TISSUE=Liver;  
RX MEDLINE=96079109; PubMed=8530072;  
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;  
RT "The mouse angiogenin gene family: structures of an angiogenin-related  
protein gene and two pseudogenes.";  
RL Genomics 29:200-206(1995).  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U22519; AAA91367.1; -  
DR HSSP: P03950.1AAY.  
DR MCD: MGI104984; Angrp.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PF00074; RNaseA.1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR ProDom: PD000535; RNaseA.1.  
DR SMART: SM00092; RNase\_Pc.1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC.1.  
KW Signal; Hydrolase; Nuclease; Endonuclease.  
FT SIGNAL 1 24  
FT CHAIN 25 145 ANGIOENIN-RELATED PROTEIN.  
FT MOD\_RES 25 25 PYROGLUTAMINE CARBOXYLIC ACID (BY  
FT ACT\_SITE 37 37 SIMILARITY).  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 137 137 BY SIMILARITY.  
FT DISULFID 50 104 BY SIMILARITY.  
FT DISULFID 63 115 BY SIMILARITY.  
FT DISULFID 81 130 BY SIMILARITY.  
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429CAD CRC64;  
Query Match 20.9%; Score 121.5; DB 1; Length 145;  
Best Local Similarity 36.8%; Pred. No. 2.3e-06;  
Matches 28; Conservative 11; Mismatches 30; Indels 7; Gaps 3;  
QY 31 CKDKNTFTYRPREYKAIC--KGIASKNV-LTFEFLYSDCNVTSR---PCKYKILKS 83  
DB 63 CKDVNTFTYRPREYKAIC--KGIASKNV-LTFEFLYSDCNVTSR---PCKYKILKS 122  
DB 84 TTFECVTCENQAPYHF 99  
DB 123 FRTIITCENGWPHVF 138  
RESULT 7  
ANGI\_CERAE STANDARD; PRT; 146 AA.  
AC Q8WNG6;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).  
GN ANG OR RNASE5.  
OS Cercopithecus aethiops (Green monkey) (Givet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
OC Cercopithecoidea; Cercopithecus.  
OX NCBI\_TaxID=9534;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in  
RT primate evolution.";  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS  
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,  
CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY  
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL  
CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND  
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY  
CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AF441664; AL61646.1; -  
DR KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;  
KW Protein synthesis inhibitor; Signal.  
FT SIGNAL 1 24  
FT CHAIN 25 146 ANGIOENIN.  
FT MOD\_RES 25 25 PYROGLUTAMINE CARBOXYLIC ACID (BY  
FT ACT\_SITE 37 37 SIMILARITY).  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 138 138 BY SIMILARITY.  
FT DISULFID 50 105 BY SIMILARITY.  
FT DISULFID 63 116 BY SIMILARITY.  
FT DISULFID 81 131 BY SIMILARITY.  
SQ SEQUENCE 146 AA; 16444 MW; 27860112E85B80F9 CRC64;  
Query Match 20.9%; Score 121.5; DB 1; Length 146;  
Best Local Similarity 29.7%; Pred. No. 2.3e-06;  
Matches 30; Conservative 17; Mismatches 31; Indels 23; Gaps 4;  
QY 6 TPOKHLTNRDVCNNILSTNLFHCKDKNTFTYRPREYKAIC--KGIASKNV-LTT 61  
DB 53 TMRRLHTSP-----CKDINTFTYRPREYKAIC--KGIASKNV-LTT 97  
QY 62 FEFLYSDCNVTSR---RPCKYKILKSTYTCVTCENQAPYHF 98  
DB 98 SPFOVNTCNLRGSGSPRCQYRATRGSRNIVGCEGLPVH 138  
RESULT 8  
RNP\_GALMU STANDARD; PRT; 124 AA.  
AC P00680;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).  
GN RNASE1 OR RN51.  
OS Galea musteloides (Cuis).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Galea.  
OX NCBI\_TaxID=10146;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=87036770; PubMed=6571219.



Db	47	DEYCSNMKNNRLTRPCKXDRNTEHGNKNNDIKAICEDNRNGQYRDLRISKS-----EPQ	101
Oy	66	LSDC---NVTSR-PCKYKLKSTITFCYTCENQAPVHF	99
Db	102	ITICHKGGSSRPCKRGATEDSRVIVGCEGDLPHVF	139
	RESULT 10		
	RNBP_CAVPO		
ID	RNBP_CAVPO	STANDARD:	PRT: 128 AA.
AC	P00679:		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).		
OS	Cavia porcellus (Guinea pig)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; HystriCognathI; Cavillidae; Cavia.		
NCBI	TaxId=10141;		
RN	(1)		
RP	SEQUENCE.		
RC	TISSUE=Pancreas;		
RX	MEDLINE=77185023: PubMed=862624:		
RA	van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastra W.,		
RA	Beutema J.J.;		
RT	"Guinea-pig pancreatic ribonucleases. Isolation, properties, primary		
RT	structure and glycosylation.";		
RL	Eur. J. Biochem. 75:91-100(1977).		
CC	-I- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-		
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P		
CC	with 2',3'-cyclic phosphate intermediates.		
CC	-I- SUBCELLULAR LOCATION: Secreted.		
CC	-I- TISSUE SPECIFICITY: PANCREAS.		
CC	-I- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.		
DR	PIR: A00826: NRGPB.		
DR	HSSP: P00656: 1SRN.		
DR	InterPro: IPR001427: RNaseA.		
DR	Pfam: PF00074: rnasea, 1.		
DR	PRINTS: PR00794: RIBONUCLEASE.		
DR	ProDom: PD000535: RNaseA; 1.		
DR	SMART: SM00092: RNase_PC; 1.		
DR	PROSITE: PS00127: RNASE_PANCREATIC; 1.		
KW	Hydrophobic; Nuclease; Endonuclease; Glycoprotein.		
FT	DISULFID	26	84
FT			BY SIMILARITY.
FT	DISULFID	40	95
FT			BY SIMILARITY.
FT	DISULFID	58	110
FT			BY SIMILARITY.
FT	DISULFID	65	72
FT			BY SIMILARITY.
FT	ACT_SITE	12	12
FT			BY SIMILARITY.
FT	ACT_SITE	41	41
FT			BY SIMILARITY.
FT	ACT_SITE	119	119
FT			BY SIMILARITY.
FT	CAROHND	21	21
FT			N-LINKED (GLCNAC. . .)
FT	CAROHND	34	34
FT			N-LINKED (GLCNAC. . .)
FT	VARLANT	64	64
FT			L -> P.
SEQ	SEQUENCE	128 AA: A2P4101A1A13E93B	CRC64:
	Query Match	19.8%:	Score 115; DB 1; Length 128;
	Best Local Similarity	25.9%:	Pred No. 1e-05; Indels 22; Gaps 7
	Matches	30; Conservative	25; Mismatches 39;
Oy	5	LTFQKRL-----NTRDVCNNIL---STNLFHCKDKNTEFYISRPPEVKAIC--KGII	53
Db	6	MKFORQHMDDPEGSPENSNNY-CNVAMIRRMNQGRCKPVPNTFVHESLADYQAVCPQKNVL	64
Oy	54	ASKNVLTFFERY-----LSDCANTSRP-----CKYKLKSTITFCYTCENQ--APVHF	99
Db	65	CKNGGTNCYQSYSRMRITDCRVTSKKEPNCYSRMSQAQKSLIIVACGDDPYVPVHF	120
	RESULT 11		
ID	RNP_MYOCO		
AC	P00676:	STANDARD:	PRT: 128 AA.
DT	21-JUL-1986 (Rel. 01, Created)		

DT	21-JUL-1986 (Rel. 01, Last sequence update)
DE	15-JUN-2002 (Rel. 41, Last annotation update)
GN	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS	Myocastor coypus (Coypu) (Nutria).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Hystriognathi; Myocastoridae;
CC	Myocastor.
CC	NCBI_Taxid=10157;
CC	(1)
CC	SEQUENCE.
CC	TISSUE=Pancreas;
CC	MEDLINE=77065676; PubMed=999896;
CC	van den Berg A., van den Hende-Timmer L., Beintema J.J.;
CC	"Isolation, properties and primary structure of coypu and chinchilla
CC	pancreatic ribonuclease.";
CC	Biochim. Biophys. Acta 453:400-409(1976).
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC	with 2',3'-cyclic phosphate intermediates.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: PANCREAS.
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC	PIR: A00822; NRCU.
CC	HSSP: P00656; 1SRN.
CC	InterPro: IPR001427; RNaseA.
CC	Pfam: PF00074; rnasea; 1.
CC	PRINTS: PR00794; RIBONUCLEASE.
CC	Prodom: P000535; RNaseA; 1.
CC	SMART: SM0092; RNase.Pc; 1.
CC	PROSITE: PS00127; RNASE_PANCREATIC; 1.
CC	KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
CC	FT DISULFID 26 84 BY SIMILARITY.
CC	FT DISULFID 40 95 BY SIMILARITY.
CC	FT DISULFID 58 110 BY SIMILARITY.
CC	FT DISULFID 65 72 BY SIMILARITY.
CC	FT ACT_SITE 12 12 BY SIMILARITY.
CC	FT ACT_SITE 41 41 BY SIMILARITY.
CC	FT ACT_SITE 119 119 BY SIMILARITY.
CC	FT CARBOHD 34 34 N-LINKED (GLCNAC...).
CC	SEQUENCE 128 AA; 14267 MW; 4EB924E5B445832 CRC64;
CC	Query Match 19.6%; Score 114; DB 1; Length 128;
CC	Best Local Similarity 28.2%; Pred. No. 1.3e-05;
CC	Matches 33; Conservative 19; Mismatches 37; Indels 28; Gaps 7;
CC	OY 7 FOKKHL-----TNRDVCNNIL-STNLF--HCKDKNFEITSRPEPVKALGKIASKNV 58
CC	DB 8 FEROHMSRGSPTSTPNYCNEMKSRNMTGCRKPVNFVEHPLADVAVC---FOKNV 63
CC	OY 59 L-----TTFEEYLSDCNVTSRP---CKYKLKSTTTFCTVCENQ---APVHF 99
CC	DB 64 LCKNGQTCYGSNSNMHTIDCRVTSNSDYPKCSYRTSGEENSIVACGNGPYVPVHF 120
CC	RESULT 12
CC	RNP_BALAC
CC	ID RNP_BALAC STANDARD: PRT: 124 AA.
CC	P00673:
CC	21-JUL-1986 (Rel. 01, Created)
CC	21-JUN-1986 (Rel. 01, Last sequence update)
CC	15-JUN-2002 (Rel. 41, Last annotation update)
CC	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
CC	GN RNASE1 OR RNS1.
CC	Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
CC	Balaenopteridae; Balaenoptera.
CC	NCBI_Taxid=9767;
CC	(1)
CC	SEQUENCE.
CC	MEDLINE=76277855; PubMed=962870;
CC	Emmens M., Weiling G.W., Beintema J.J.;

"The amino acid sequence of pike-whale (lesser-tongual) pancreatic ribonuclease.";  
RL Biochem. J. 157:317-323(1976).  
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: PANCREAS.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.  
DR PIR: A00818; NEMHK.  
DR HSSP: P00656; 1SRN.  
DR InterPro: IPR001427; RNaseA.  
DR Pfam: PFC0074; RNaseA\_1.  
DR PRINTS: PR00794; RIBONUCLEASE.  
DR ProDom: PD000535; RNaseA\_1.  
DR SMART: SM00092; RNase\_Pc\_1.  
DR PROSITE: PS00127; RNASE\_PANCREATIC\_1.  
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.  
FT DISULFID 26 84 BY SIMILARITY.  
FT DISULFID 40 95 BY SIMILARITY.  
FT DISULFID 58 110 BY SIMILARITY.  
FT DISULFID 65 112 BY SIMILARITY.  
FT ACT\_SITE 12 12 BY SIMILARITY.  
FT ACT\_SITE 41 41 BY SIMILARITY.  
FT ACT\_SITE 119 119 BY SIMILARITY.  
FT CARBOHYD 76 76 N-LINKED (GLCNAC, . . .) IN 30% OF THE MOLECULES.  
SO SEQUENCE 126 AA; 14125 MW; F57475459F697E20 CRC64;  
Query Match 19.4%; Score 113; DB 1; Length 124;  
Best Local Similarity 26.9%; Pred. No. 1.6e-05;  
Matches 32; Conservative 16; Mismatches 43; Indels 28; Gaps 6;  
QY 5 LTFQKHLNTRDYVD-----CNNILSTNLF--HCKDKNFTYSRPEPYKAICGIIASK 56  
DB 6 MRFQROHMDGNSPGNNPNYCNQMMRRKKTGRCRPFVTFVHESLEDAVAC---SQR 61  
57 NVL-----TTFEYLDSCNVTSRP---CKYKIKKSTITFCVTCENQ--APVHF 99  
62 NVLCNKGRTNCEYNSNTMHTDCRQCGSSKYPKCAKTSQKKEHIIYACGNGYVPHF 120  
RESULT 13  
ANGI\_MACMU STANDARD: PRT: 146 AA.  
AC O8MN63:  
DT 15-JUN-2002 (rel. 41, Created)  
DT 15-JUN-2002 (rel. 41, Last sequence update)  
DE Angiogenin precursor (EC:3.1.27.-) (Ribonuclease 5) (Rnase 5).  
GN ANG OR RNASE5.  
OS Macaca mulatta (Rhesus macaque).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.  
OX NCBI\_TaxId=9544;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21918422; PubMed=11919285;  
RA Zhang J., Rosenberg H.F.;  
RT "Diversifying selection of the tumor-growth promoter angiogenin in RT primate evolution."  
RL Mol. Biol. Evol. 19:438-445(2002).  
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

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CC -1- send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
DR EMBL: AF41667; AAL61649.1;  
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;  
KW Protein synthesis inhibitor; Signal.  
FT SIGNAL 1 24 BY SIMILARITY.  
FT CHAIN 25 146 ANGIOGENIN.  
FT MOD\_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).  
FT ACT\_SITE 37 37 BY SIMILARITY.  
FT ACT\_SITE 64 64 BY SIMILARITY.  
FT ACT\_SITE 138 138 BY SIMILARITY.  
FT DISULFID 50 105 BY SIMILARITY.  
FT DISULFID 63 116 BY SIMILARITY.  
FT DISULFID 81 131 BY SIMILARITY.  
SO SEQUENCE 146 AA; 16301 MW; E39A89215DB2A244 CRC64;  
Query Match 19.3%; Score 112.5; DB 1; Length 146;  
Best Local Similarity 27.7%; Pred. No. 2.2e-05;  
Matches 28; Conservative 17; Mismatches 33; Indels 23; Gaps 4;  
QY 6 TPOKHLNTRDYVDNINILSTNLFHCKDKNFTYSRPEPYKAIC--GIIASKNV-LTP 61  
DB 53 TMRRHILTS-----CKDINTFVGNHHTALCGDENGSPYCGNLRIST 97  
QY 62 FEFYLDSCNVTSRP---RPCKYKIKKSTITFCVTCENQAPVH 98  
DB 98 SPFOYTTCKLRGSGPPRCQYRATRGSRNIVGCGENGLPVH 138  
RESULT 14  
ANGI\_MOUSE STANDARD: PRT: 145 AA.  
AC P21570;  
DT 01-MAY-1991 (rel. 18, Created)  
DT 01-MAY-1991 (rel. 18, Last sequence update)  
DT 15-JUN-2002 (rel. 41, Last annotation update)  
DE Angiogenin precursor (EC 3.1.27.-).  
GN ANG.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91025023; PubMed=2222458;  
RA Bond M.D., Vallee B.L.;  
RT "Isolation and sequencing of mouse angiogenin DNA."  
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).  
RN [2]  
RP PARTIAL SEQUENCE.  
RC TISSUE=Serum;  
RX MEDLINE=93192291; PubMed=8448182;  
RA Bond M.D., Strydom D.J., Vallee B.L.;  
RT "Characterization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and RT regions."  
RL Biochim. Biophys. Acta 1162:177-186(1993).  
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

